

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/566,054
Source: IFWP
Date Processed by STIC: 02/07/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/10/566,054

TIME: 13:53:23

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\02012006\J566054.raw

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3 <110> APPLICANT: Ambrose, Helen Jean
4   March, Ruth
6 <120> TITLE OF INVENTION: USE OF POLYMORPHISMS IN HUMAN OATP-C ASSOCIATED WITH AN
EFFECT ON STATIN
7   PHARMACOKINETICS IN HUMANS IN STATIN THERAPY
9 <130> FILE REFERENCE: 06275-492US1
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/566,054
C--> 11 <141> CURRENT FILING DATE: 2006-01-25
11 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/003236
12 <151> PRIOR FILING DATE: 2004-07-26
14 <150> PRIOR APPLICATION NUMBER: GB 0317592.4
15 <151> PRIOR FILING DATE: 2003-07-26
17 <160> NUMBER OF SEQ ID NOS: 5
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 691
23 <212> TYPE: PRT
24 <213> ORGANISM: Homo Sapiens
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33           20           25           30
36 Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
37           35           40           45
40 Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
41           50           55           60
44 Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
45 65           70           75           80
48 Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
49           85           90           95
52 Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
53           100          105          110
56 Leu Pro His Phe Phe Met Gly Tyr Arg Tyr Ser Lys Glu Thr Asn
57           115          120          125
60 Ile Asn Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
61           130          135          140
64 Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
65 145          150          155          160
68 Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
69           165          170          175
72 Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
73           180          185          190
76 Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr

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81          210          215          220
84 Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
85 225          230          235          240
88 Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
89          245          250          255
92 Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
93          260          265          270
96 Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys
97          275          280          285
100 Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu
101          290          295          300
104 Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys
105 305          310          315          320
108 Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro
109          325          330          335
112 Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr
113          340          345          350
116 Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly
117          355          360          365
120 Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro
121          370          375          380
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125 385          390          395          400
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129          405          410          415
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133          420          425          430
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137          435          440          445
140 Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn
141          450          455          460
144 Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
145 465          470          475          480
148 Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys
149          485          490          495
152 Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu
153          500          505          510
156 Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp
157          515          520          525
160 Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn
161          530          535          540
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165 545          550          555          560
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169          565          570          575
172 Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly
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176 Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly
 177 595 600 605
 180 Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val
 181 610 615 620
 184 Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr
 185 625 630 635 640
 188 Ile Ile Leu Ile Tyr Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile
 189 645 650 655
 192 Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser
 193 660 665 670
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 197 675 680 685
 200 Thr His Cys
 201 690

204 <210> SEQ ID NO: 2

205 <211> LENGTH: 2050

206 <212> TYPE: DNA

207 <213> ORGANISM: Homo Sapiens

209 <400> SEQUENCE: 2

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214	taaggcactt	tacatacact	aatctttat	tccaaatata	gacttcttac	tttatagatg		180
216	agtgcactga	tgctcagaaa	tggtaaataa	cctactgatg	tttatactgc	tggtcaggtag		240
218	cagagacata	tcggcattta	agtctttcag	acttcaaagg	ccatgatatt	tcacagagc		300
220	tgtgatagcc	gttcttgaaa	aaaatatcag	ctgattcttt	aatcaatttt	ttgtcatcta		360
222	actgatgcgt	ggctgttagc	ataatattga	tcttgaaaga	tgttttgcaa	catctttccc		420
224	ctgggtgact	cttgtttttc	catgatccca	caaatgagc	agtctaatta	tttacacaat		480
226	taggaagaga	aaagggggcac	agagaatgct	ctttgacctc	tgaaaatatt	ggagaatttt		540
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230	ttcattgtat	ataatatata	tattagtctc	caaacatggt	gatgtgtttt	caatgaaatg		660
232	gatgtctgag	gagaaaaacca	ttagcctgag	aaaacccaaa	ctgtattccc	attgtgaata		720
234	aaaggaagtc	cataaaaaatg	atggaaaatg	ttctgcattc	ctgttatgat	atcaaaatct		780
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238	gccagaatct	gctgggtatg	ggactggatt	gctattttga	caactcgcca	gtagattctt		900
240	actcagcaga	gtatttggaa	gccttactct	aatatttttg	ccttggttct	acattttctca		960
242	gttctgcaca	gtcattcttc	ccctctacac	tactctttag	tttgtctcat	gattccaata		1020
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246	atacattttg	ctgcaaccat	atcaacaaat	gtcccatgaa	tgataagggg	taaccatatt		1140
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254	taatgtccaa	ggtataattg	agagtctaaa	atgtttgagt	tattgaatta	attaaacttc		1380
256	atctctactc	aagaaaactt	ttaactgagt	taagctcttc	ctttctccac	aagtcaagtc		1440
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260	ataaaagcagt	cttaattttc	atcattcaga	aaaatgggtct	tgagtttaatt	tggtgactctc		1560
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291 tctatatttc aatcatggac caaaatcaac atttgaataa aacagcagag gcacaacctt 180
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359 ataaacattt tgtcccttct gctggggcag atagtgaac acattgttaa ggggagaaaa 2220
361 aaagccactt ctgcttctgt gtttccaaac agcattgcac tgattcagta agatgttatt 2280
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369 tgagagacat gggtactgtg taataaaaga aaaaatactt gttcaggtaa ttctaattct 2520
371 taataaaaca aatgagtatc atacaggtag aggttaaaaa ggaggagcta gattcatatc 2580
373 ctaagtaaag agaaatgcct agtgtctatt ttattaaaca aacaaacaca gagtttgaac 2640
375 tataatacta aggcctgaag tctagcttgg atatatgcta caataatatc tgttactcac 2700
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385 <211> LENGTH: 691
386 <212> TYPE: PRT
387 <213> ORGANISM: Homo Sapiens
389 <400> SEQUENCE: 4
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396 20 25 30
399 Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
400 35 40 45
403 Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
404 50 55 60
407 Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
408 65 70 75 80
411 Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
412 85 90 95
415 Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
416 100 105 110
419 Leu Pro His Phe Phe Met Gly Tyr Arg Tyr Ser Lys Glu Thr Asn
420 115 120 125
423 Ile Asp Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
424 130 135 140
427 Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
428 145 150 155 160
431 Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Ala Phe Met
432 165 170 175
435 Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
436 180 185 190
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440 195 200 205
443 Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date